

Fig 1

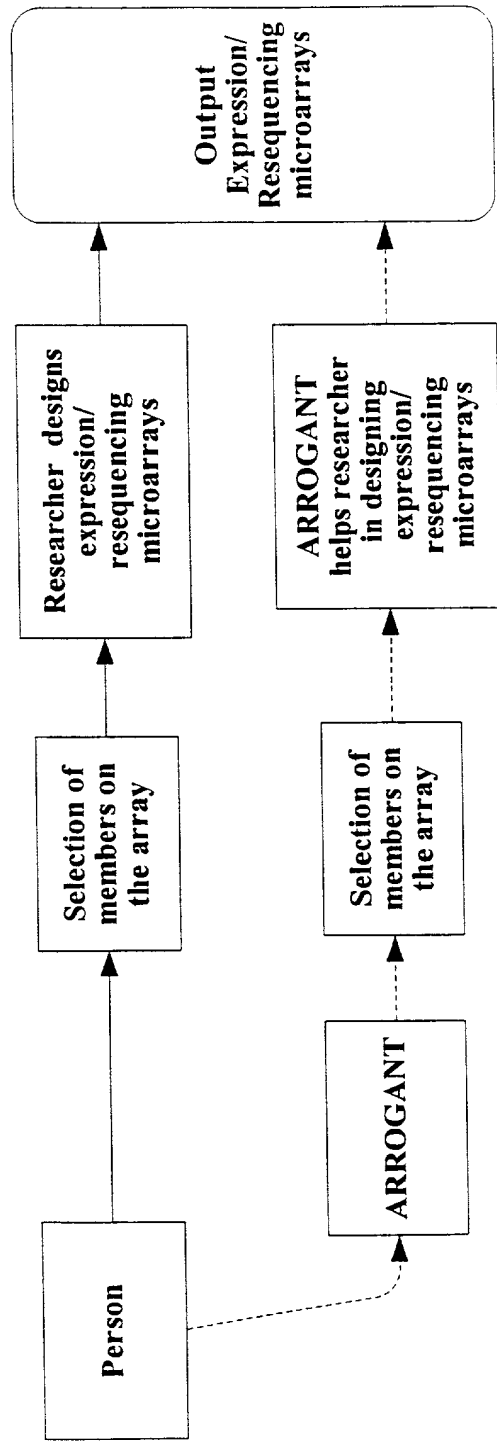


Fig 2

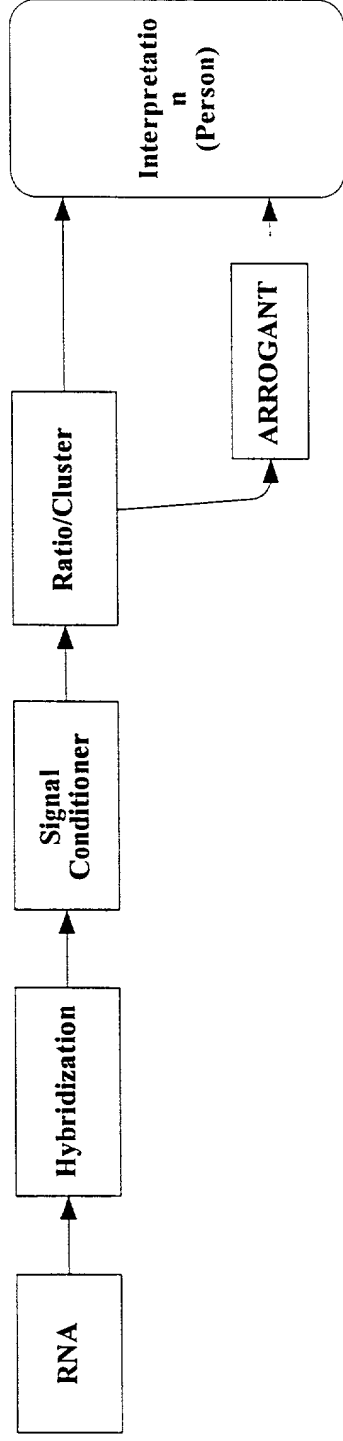


Fig 3

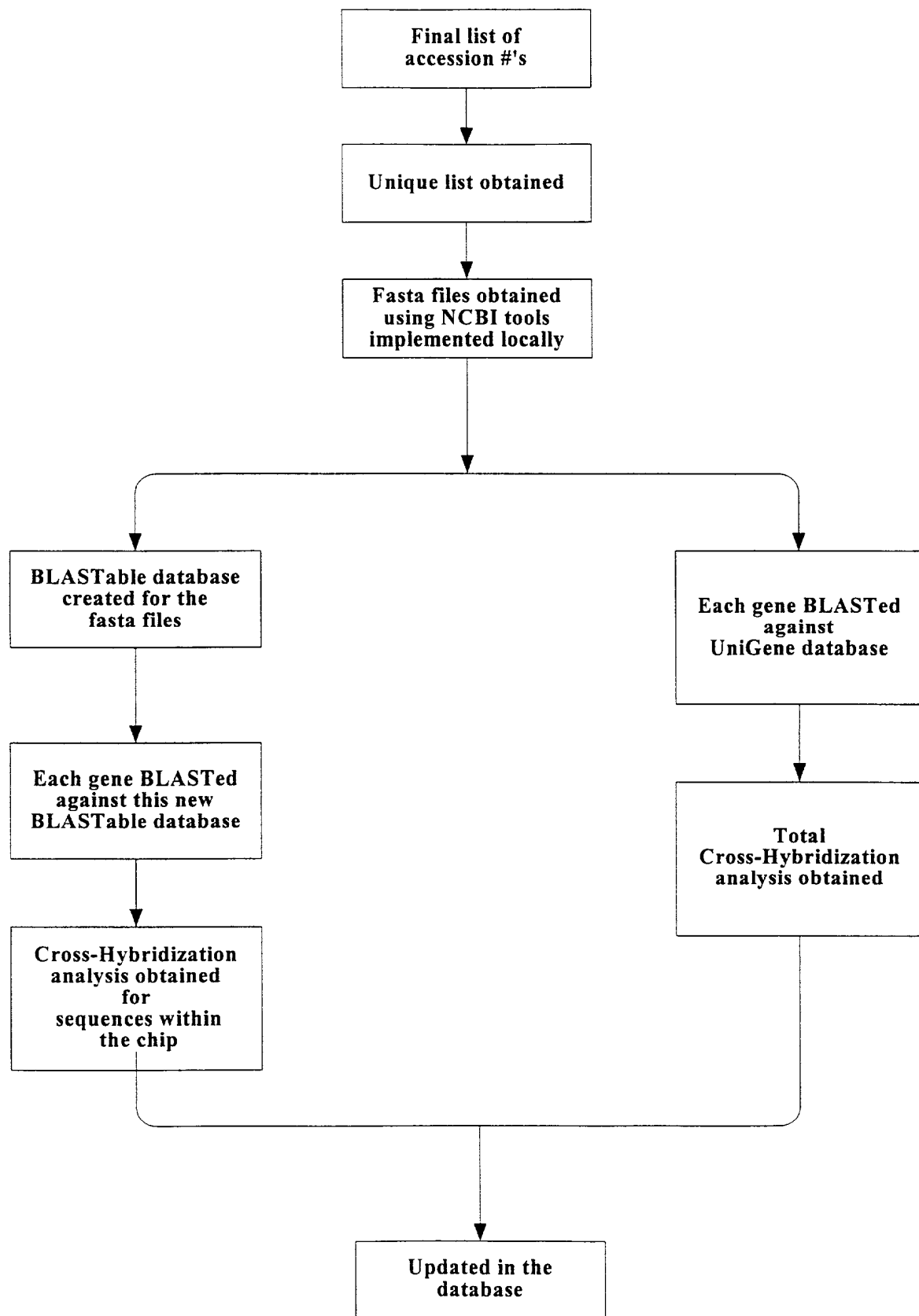


Fig 4

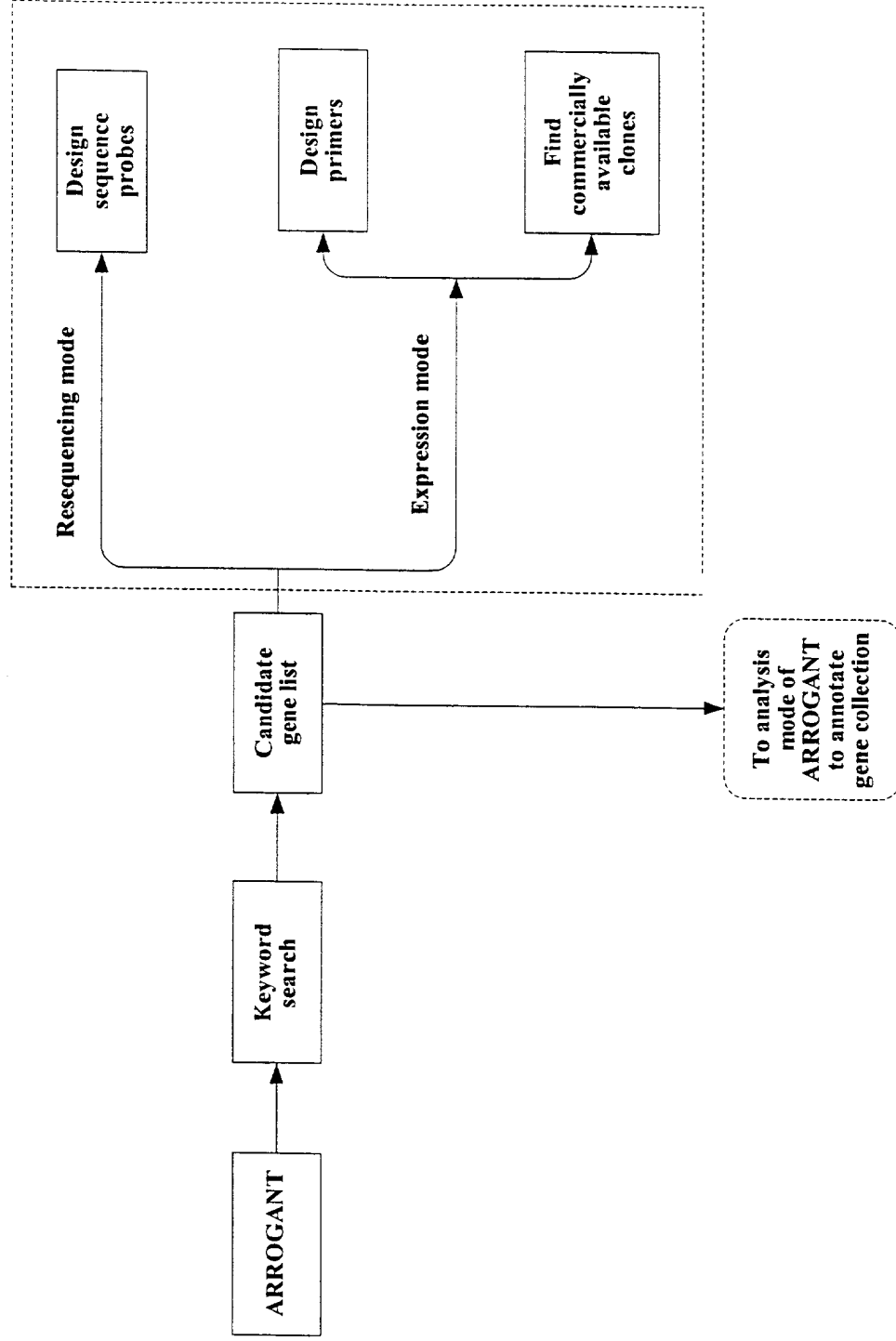


Fig 5

Address: <http://manager.suimed.edu.my/web/index.asp>

Back Forward Stop Refresh Home Search Favorites History Mail Print Edit Cancel

Links: [My Links](#) [About](#) [Business](#) [Computers](#) [Education](#) [E-Books](#) [E-Tools](#) [E-Health And Fitness](#)

Address: <http://manager.suimed.edu.my/web/index.asp>

click on Species

User Email: palke01@uqsw.suimed.edu

Array Name: [lga](#)

Number of Array Members: [110](#) Use: [r](#) Resequencing [r](#) Expression

Source: [r](#) PCR Products [r](#) 3' Exon End Only
[r](#) Clones [r](#) Random Exons
[r](#) Both

Keywords: [cardiac hypertrophy](#)

Databases:

- [r](#) GenBank
- [r](#) UniGene
- [r](#) LocusLink
- [r](#) KEGG
- [r](#) KEGG Pathway
- [r](#) Research Genetics

26/12/01 10:36:36 AM [Expand](#) [Print](#) [Close](#) [Main](#)

Fig 6

| Microsoft Internet Explorer | | | | | | | | | |
|--|--------------|---|--------------|--------------|--|--------------|--|-----------|--|
| File Edit View Favorites Tools Help | | | | | | | | | |
| Back | | Forward | | Stop | | Home | | Search | |
| My Links | | My Favorites | | My Computers | | My Documents | | My Recent | |
| Address http://anagantamed.edu/myweb/eye/eyeheader.asp | | | | | | | | | |
| GO:12345678910 | | | | | | | | | |
| Record | Accession No | Definition | Organism | | | | | | |
| 1 | A32415 | H.sapiens PAI-2 cDNA in pDBP1. | Homo sapiens | | | | | | |
| 2 | AA062310 | m164f06.r1 Stratagene mouse kidney (#937315) Mus musculus cDNA clone IMAGE:516803 5' similar to WP:C40H1.6 CE00114 ;, mRNA sequence. | Mus musculus | | | | | | |
| 3 | AA073008 | mm94c09.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:536080 5' similar to gb:M22810 Mouse androgen-regulated protein mRNA, complete cds (MOUSE);, mRNA sequence. | Mus musculus | | | | | | |
| 4 | AA073010 | mm94c11.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:536084 5' , mRNA sequence. | Mus musculus | | | | | | |
| 5 | AA073011 | mm94c12.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone IMAGE:536086 5' similar to gb:X70847 | Mus musculus | | | | | | |
| Done | | | | | | | | | |
| Status 46 127.0.0.1 53 504.54 23 11:38 AM | | | | | | | | | |

Fig 7

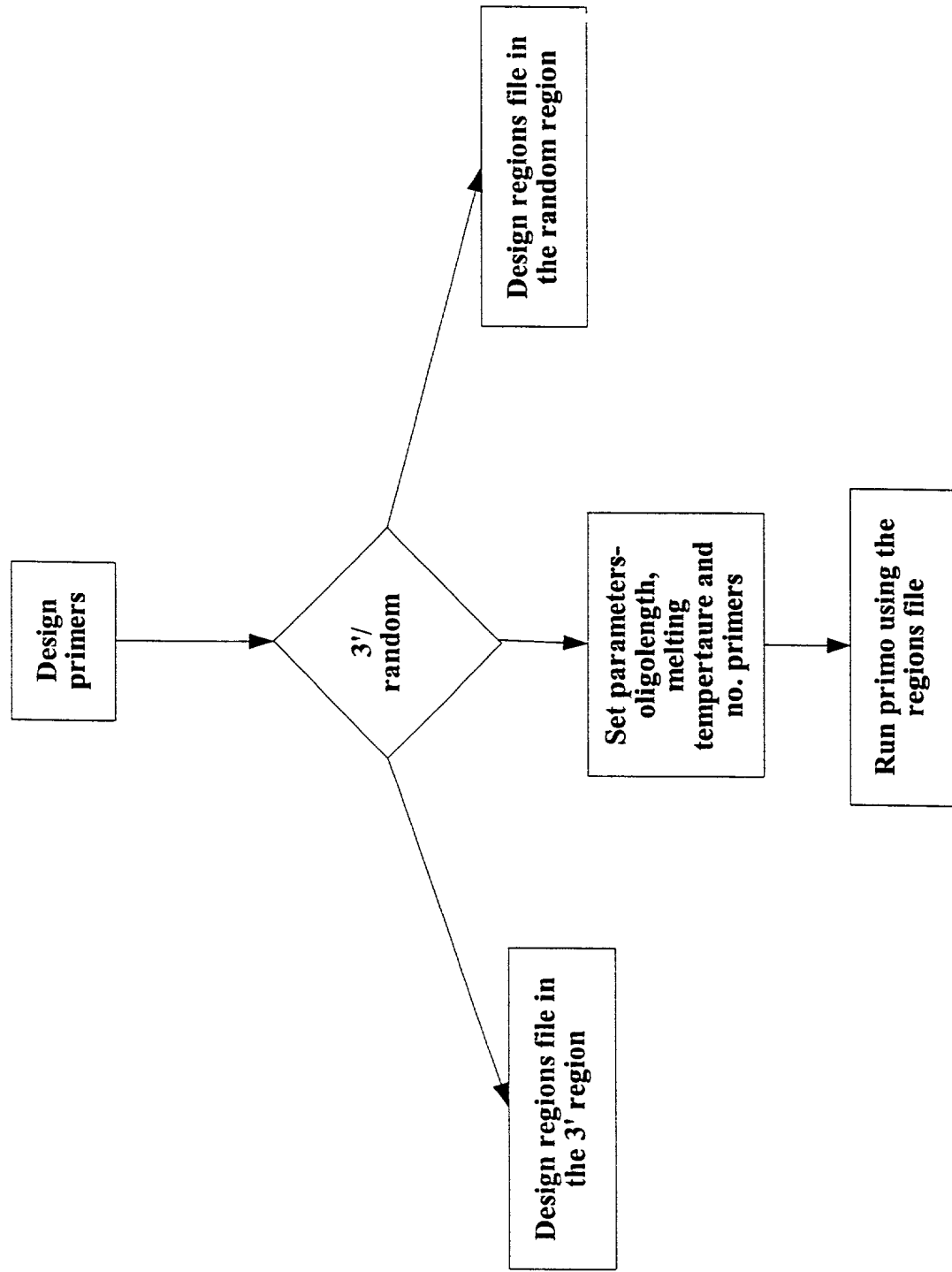


Fig 8

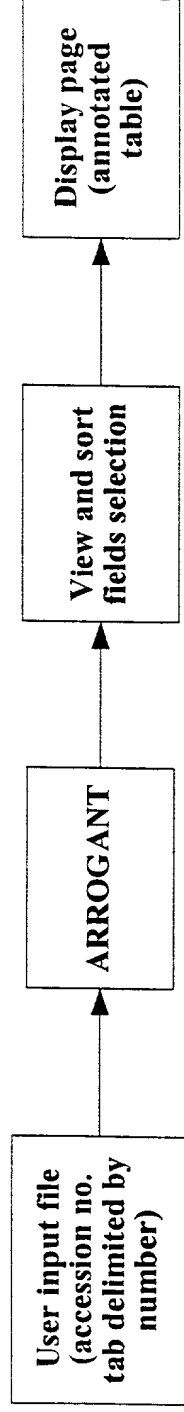


Fig 9

Select the fields you want to view, select how you would like to sort the data and press

Show Collection

| | | |
|--|---|--|
| <input type="checkbox"/> Accession | <input type="checkbox"/> IMAGE identifier | <input type="checkbox"/> Alias protein |
| <input type="checkbox"/> Expression level data | <input type="checkbox"/> Xhyb analysis | <input type="checkbox"/> Phenotype |
| <input type="checkbox"/> Unique identifier | <input type="checkbox"/> Tissues | <input type="checkbox"/> Phenotype ID/ OMIM ID |
| <input type="checkbox"/> Title | <input type="checkbox"/> GDB | <input type="checkbox"/> Chromosome |
| <input type="checkbox"/> PubMed | <input type="checkbox"/> Gene name | <input type="checkbox"/> Map location |
| <input type="checkbox"/> Related Proteins | <input type="checkbox"/> Gene Function | <input type="checkbox"/> Map link |
| <input type="checkbox"/> Related Sequences | <input type="checkbox"/> Synonyms | <input type="checkbox"/> Map type |
| <input type="checkbox"/> Taxonomy | <input type="checkbox"/> Pathway | <input type="checkbox"/> STS- marker name |
| <input type="checkbox"/> Repeats | <input type="checkbox"/> SNP analysis | <input type="checkbox"/> STS- chromosome |
| <input type="checkbox"/> Hairpin/Palindrome | <input type="checkbox"/> Unigene ID | <input type="checkbox"/> STS- ID |
| <input type="checkbox"/> Homology | <input type="checkbox"/> Locus ID | <input type="checkbox"/> Reviewed RefSeq |
| <input type="checkbox"/> Research Genetics Clone | <input type="checkbox"/> Alias symbol | <input type="checkbox"/> cDNA Source |

Sort Preferences






1. 
2. 
3. 
4. 
5. 

Fig 10

For more information on any input data field click on that link. For example, for help on Accession click on Accession

| Database | Genbank | Pomposus | Locuslink | Unigene | Research Genetics |
|--------------|----------------------|-----------------------|----------------------|-----------------------|----------------------|
| Last Updated | 2/7/01 8:06:55 AM | 1/18/01 8:35:24 AM | 2/6/01 8:34:29 AM | 1/28/01 8:34:45 AM | 1/8/01 8:35:59 AM |

Results Table

| Record | Accession | Uni ID | Cluster ID | Title | Homologs | Gene Type/Function |
|---------|-----------|---------|------------|---|-----------------------|---|
| 1 | NM_000236 | 455772 | Hs_9994 | Homo sapiens lipase, hepatic (LIPC), mRNA. | Mm.362, Rn.1195 | Summary: LIPC encodes hepatic triglyceride lipase which is expressed in liver. LIPC has dual functions of triglyceride hydrolase and ligand, bridging factor for receptor mediated lipoprotein uptake |
| 2 | NM_000023 | 4506910 | Hs_99931 | Homo sapiens sarcoglycan, alpha (50kD dystrophin-associated glycoprotein) (SGCA), mRNA. | Mm.18709, Rn.23558 | |
| Summary | 239 | 232 | 207 | 232 | 201 | 239 |
| Record | Accession | Uni ID | Cluster ID | Title | Homologs | Gene Type/Function |

Fig 11

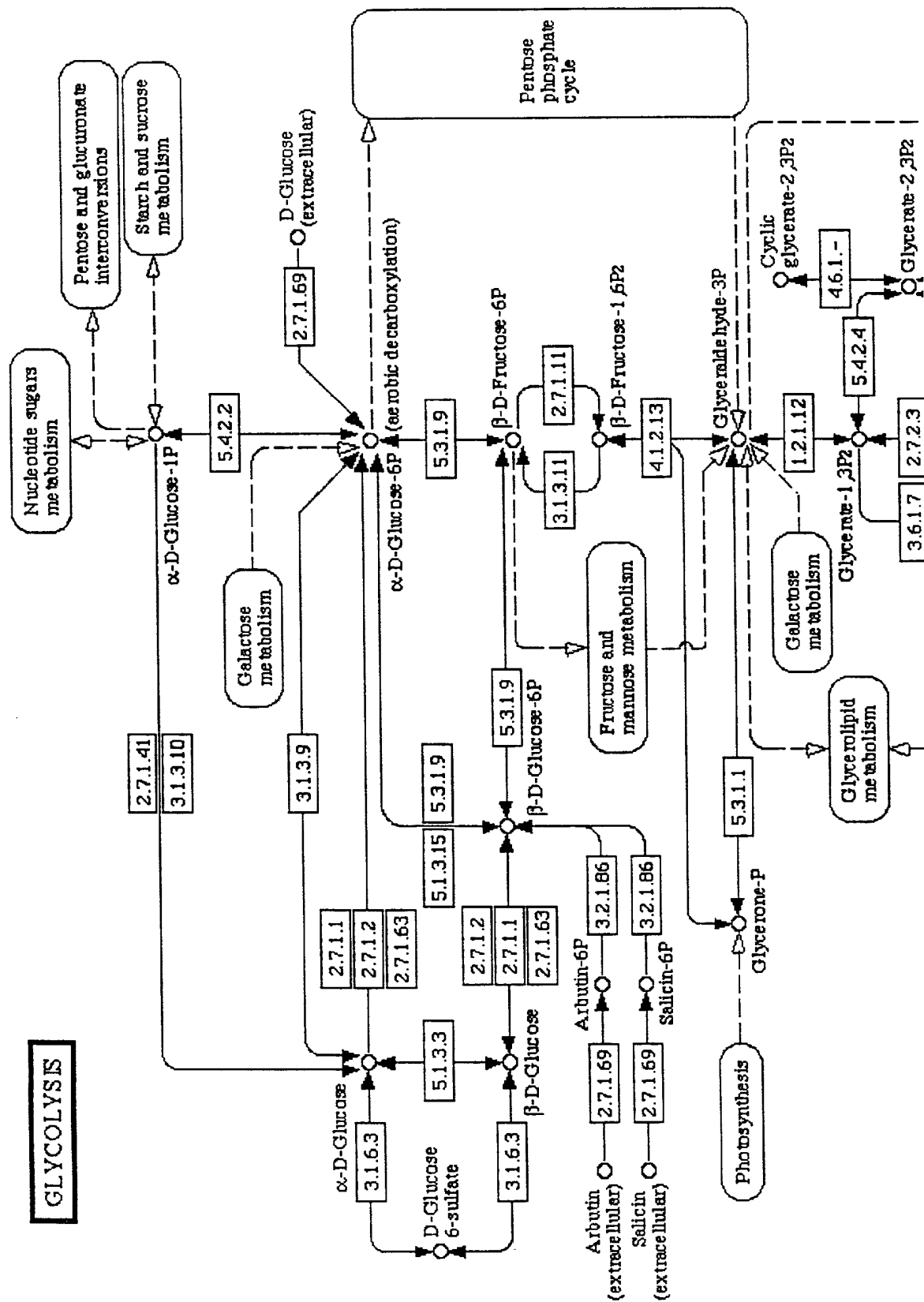


Fig 12

| Column Name | Datatype | Length | Precision | Scale | Allow Null | Default Value |
|-------------|----------|--------|-----------|-------|------------|---------------|
| accsno | varchar | 9 | 0 | 0 | | ((-1)) |
| nid | varchar | 10 | 0 | 0 | ✓ | ((-1)) |
| defn | varchar | 255 | 0 | 0 | ✓ | ((-1)) |
| type | varchar | 100 | 0 | 0 | ✓ | ((-1)) |
| dna | varchar | 6 | 0 | 0 | ✓ | ((-1)) |
| organism | varchar | 25 | 0 | 0 | ✓ | ((-1)) |
| source | varchar | 25 | 0 | 0 | ✓ | ((-1)) |
| keyword | varchar | 6 | 0 | 0 | ✓ | ((-1)) |
| comments | varchar | 255 | 0 | 0 | ✓ | ((-1)) |
| featstuff | varchar | 1400 | 0 | 0 | ✓ | ((-1)) |
| fstart | varchar | 10 | 0 | 0 | ✓ | ((-1)) |
| fend | varchar | 10 | 0 | 0 | ✓ | ((-1)) |
| species | varchar | 200 | 0 | 0 | ✓ | ((-1)) |
| authors | varchar | 255 | 0 | 0 | ✓ | ((-1)) |
| journal | varchar | 255 | 0 | 0 | ✓ | ((-1)) |
| version | varchar | 30 | 0 | 0 | ✓ | ((-1)) |
| reference | varchar | 25 | 0 | 0 | ✓ | ((-1)) |
| title | varchar | 100 | 0 | 0 | ✓ | ((-1)) |
| basepair | varchar | 10 | 0 | 0 | ✓ | ((-1)) |

Fig 13

| UNIPROT | |
|-----------|--|
| clusterid | |
| accession | |
| type | |

| UNIPROT | |
|---------|--|
| UG | |
| tissue | |

| UNIPROT | |
|-------------|--|
| clusterid | |
| otherproids | |

| UNIPROT | |
|------------|--|
| clusterid | |
| pro org | |
| pro id | |
| similarity | |

| UNIPROT | |
|------------|--|
| UG | |
| express | |
| locuslink | |
| title | |
| gene | |
| cytoband | |
| sts | |
| mqi | |
| chromosome | |

Fig 14

| | |
|----------|--|
| kegg | |
| Uniqueld | |
| Locusid | |
| Organism | |
| Name | |
| Defn | |
| class | |
| position | |
| gdb | |
| ncbi | |

| | |
|----------|--|
| lookpath | |
| pathno | |
| pathway | |

| | |
|----------|--|
| pathway | |
| Uniqueld | |
| pathno | |
| organism | |

Fig 16

| | |
|-----------|--|
| homoortho | |
| Unigid1 | |
| Unigid2 | |
| Locid1 | |
| Locid2 | |
| Acc1 | |
| Acc2 | |

Fig 17























| RG_Hs_seq_ver_101100 | |
|---|------------------|
|  | [Release Number] |
|  | [RG Plate] |
|  | [RG row] |
|  | [RG column] |
|  | [Insert Size*] |
|  | [Cluster ID] |
|  | [UG build] |
|  | [Clone ID] |
|  | Vector |
|  | Tissue |
|  | Library |
|  | Accession |
|  | NID |
|  | [Gene Name] |
|  | [Gene Symbol] |
|  | Chromosome |
|  | Band |
|  | Markers |
|  | Col019 |
|  | Barcode |
|  | Antibiotics |
|  | [repeat ?] |

Fig 18

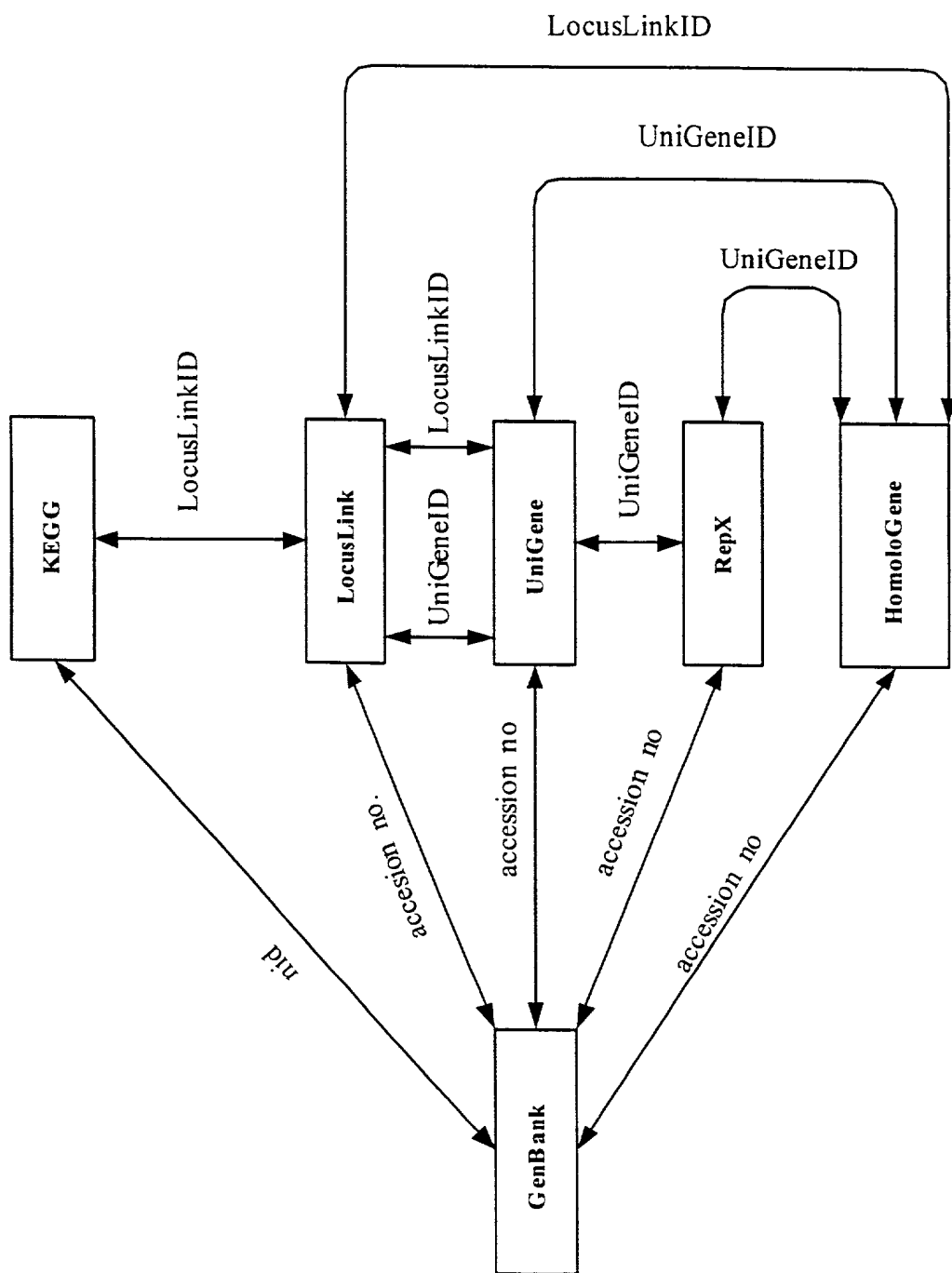


Fig 19

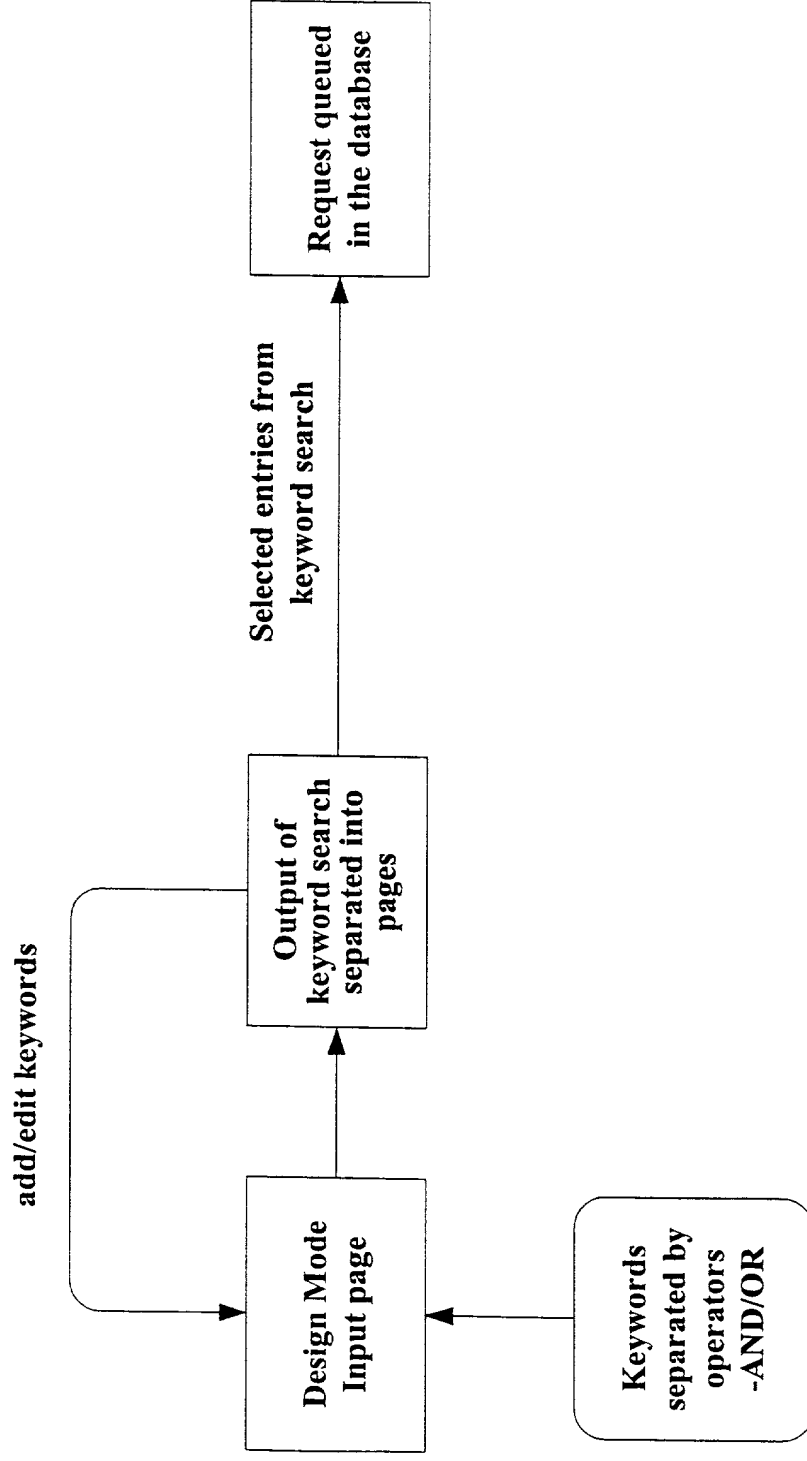
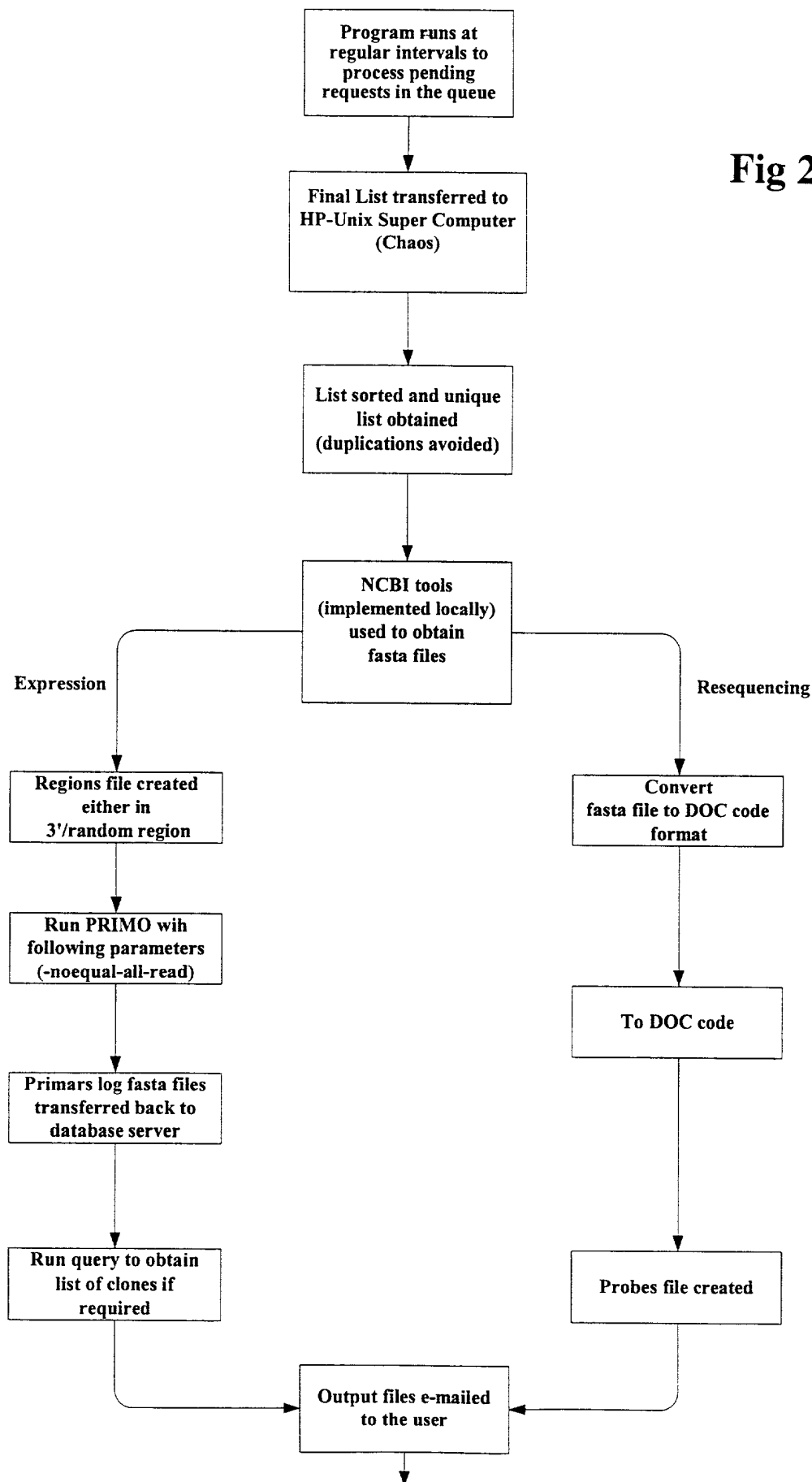
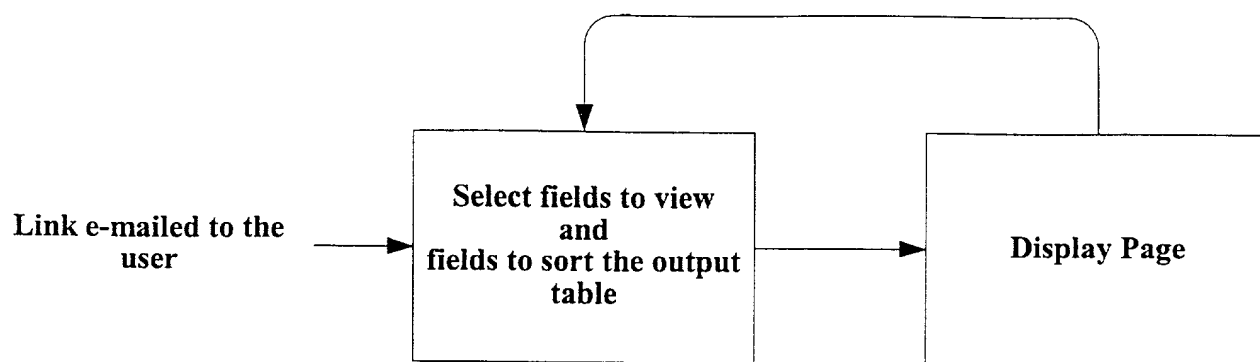


Fig 20

Fig 21





Program runs after regular intervals to process requests in the queue

Run stored procedure 'testcode'

'testcode' annotates each sequence with different items of information and stores it in the database

Cross-Hybridization analysis

Create a link using 'taskID' and e-mail it to the user

Fig 22

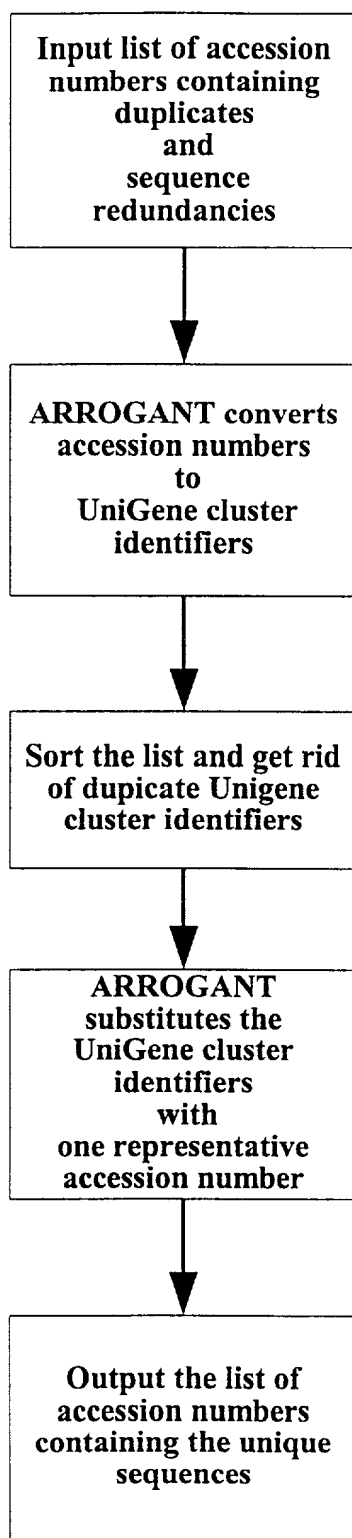


Fig 23

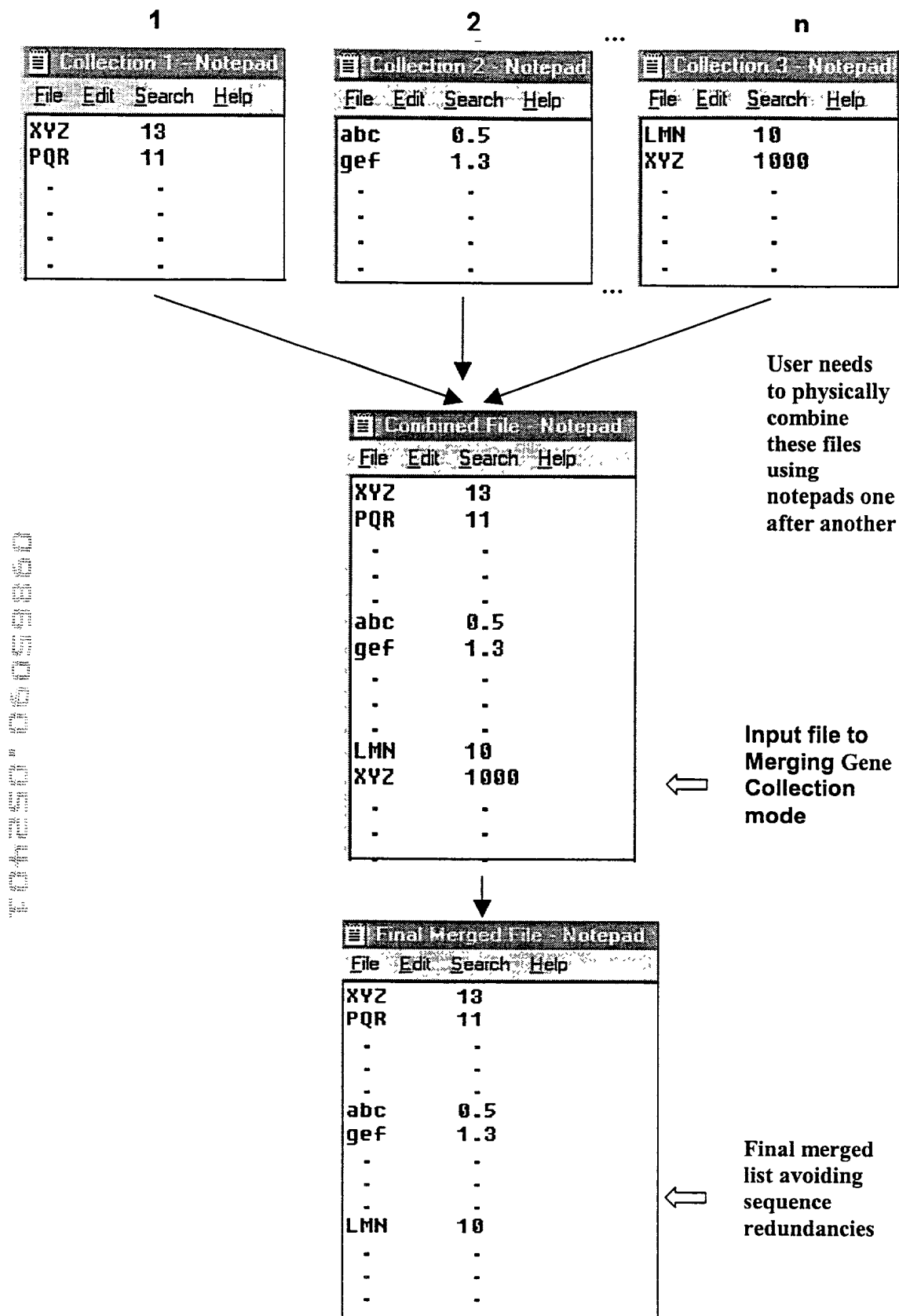


Fig 24

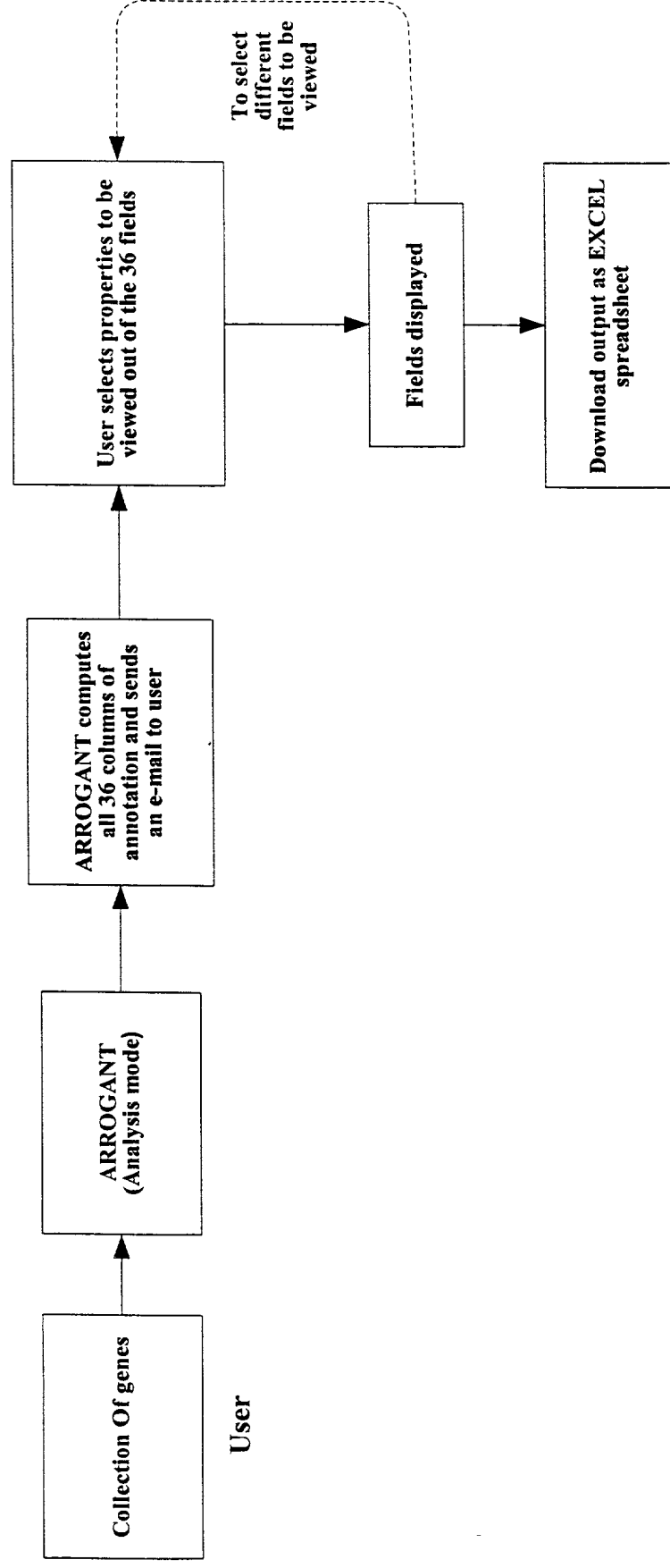


Fig 25

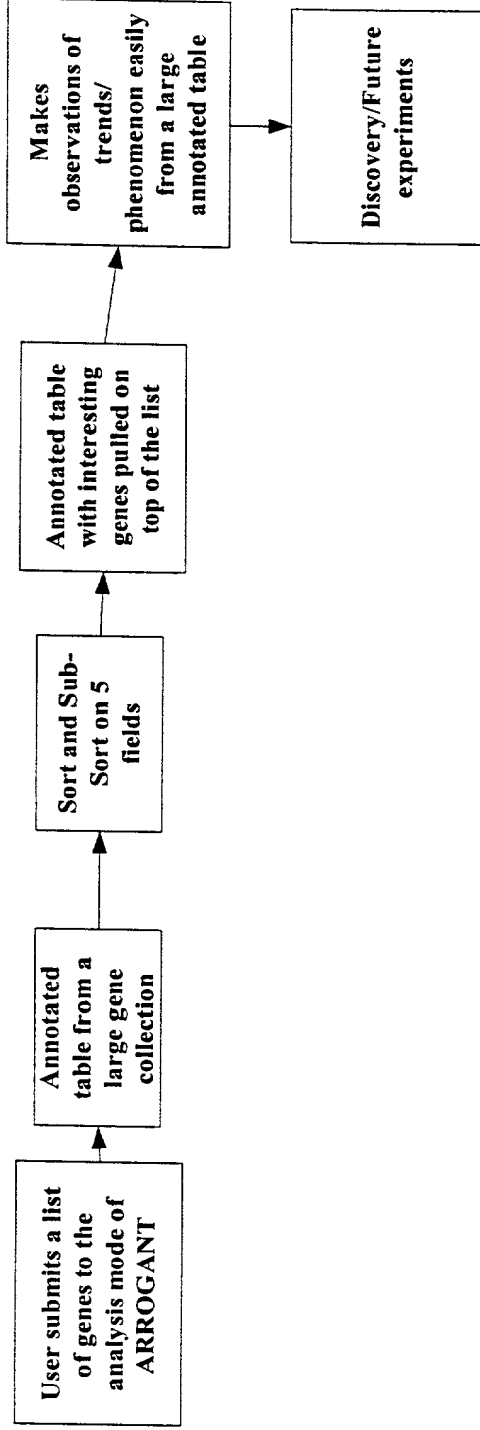


Fig 26

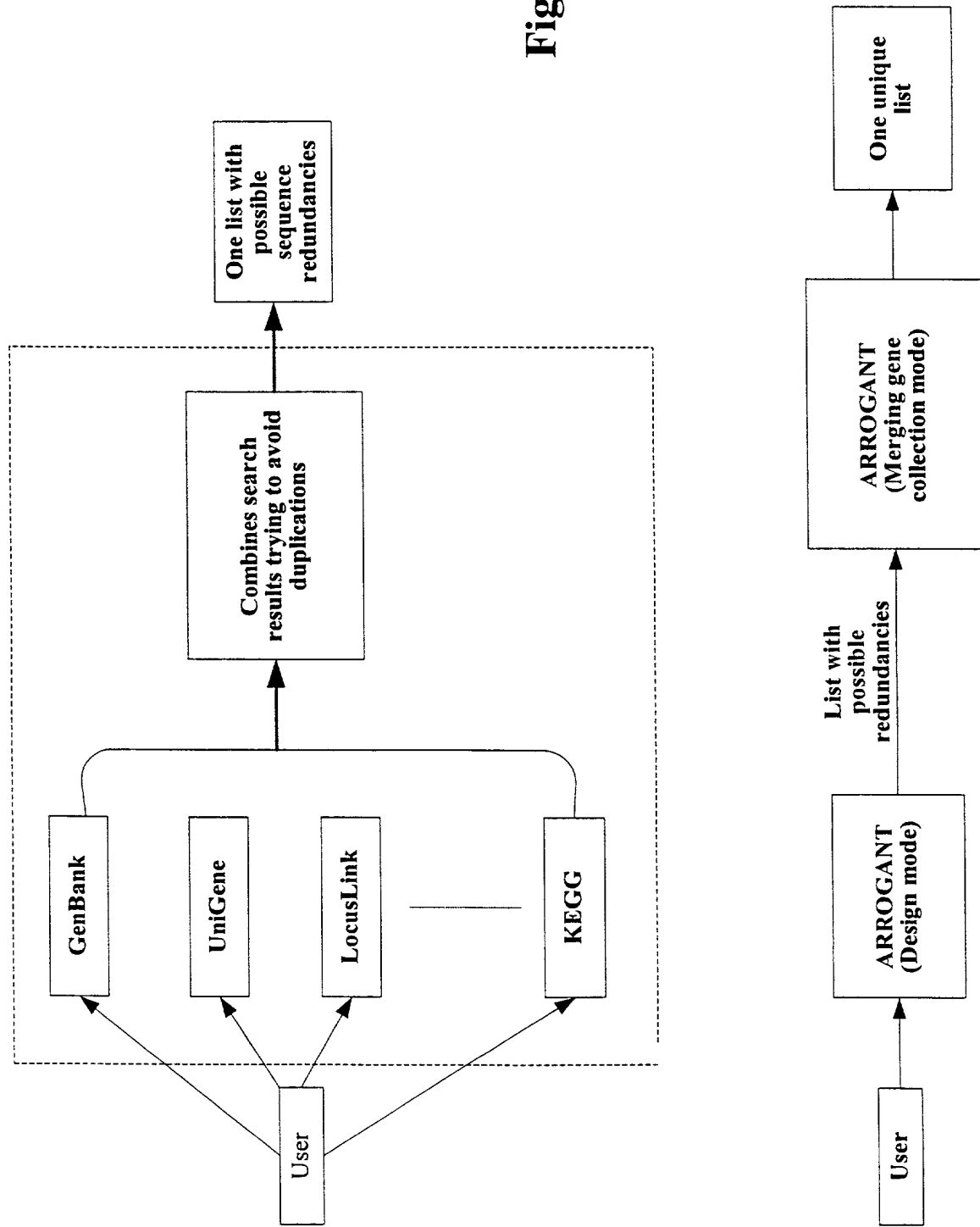


Fig 27

www.elsevier.com/locate/ymbs

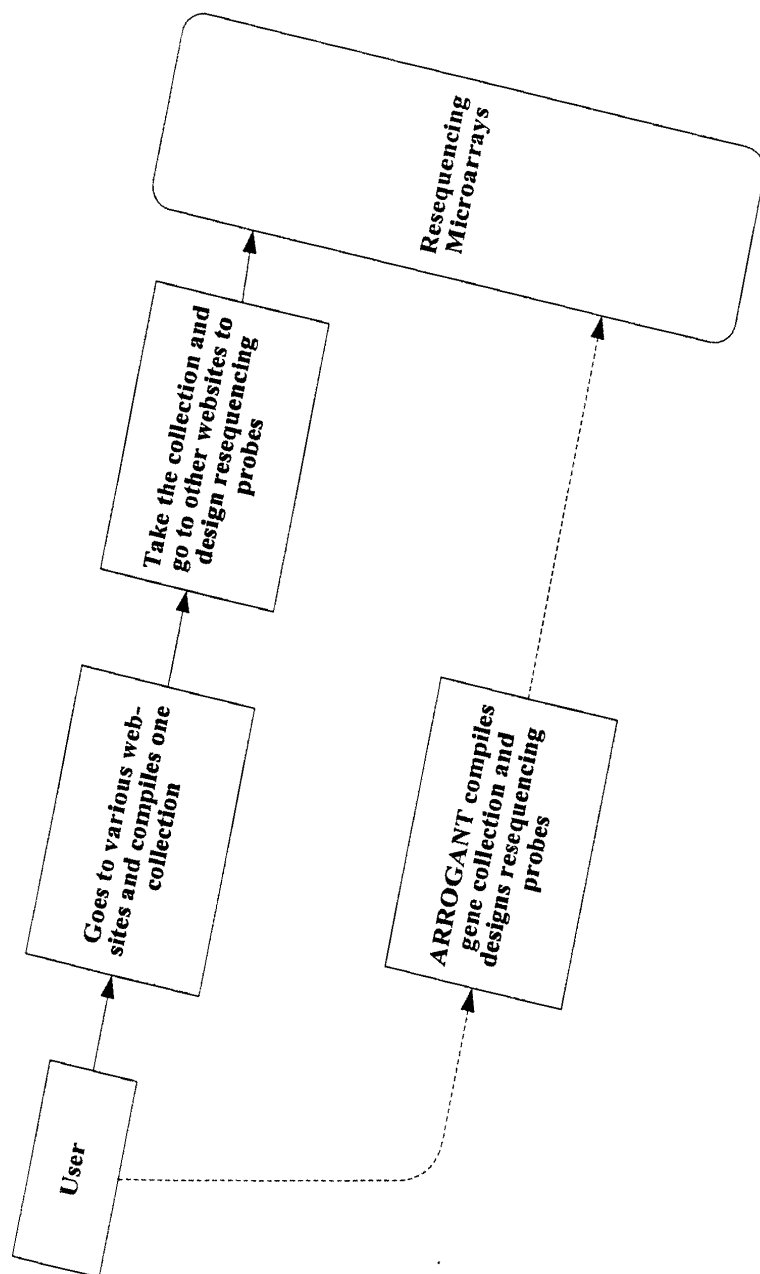


Fig 28

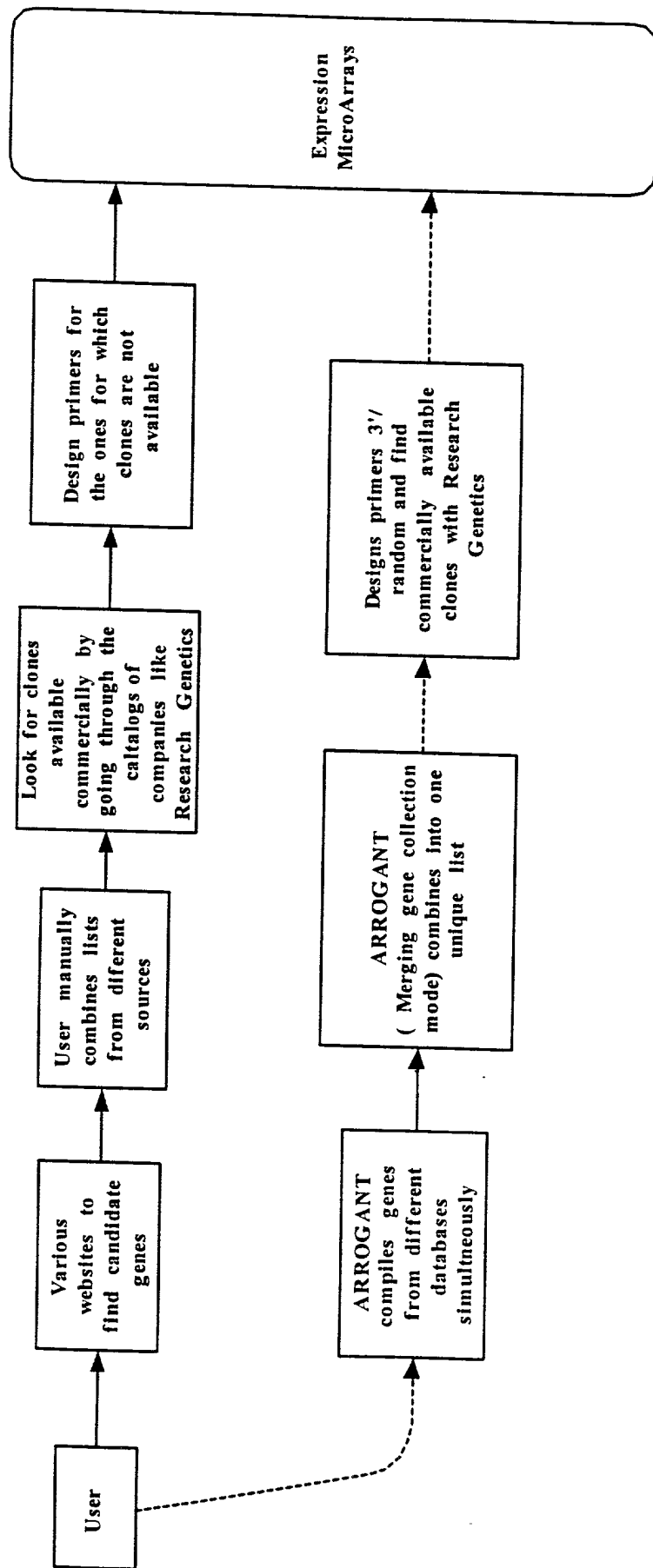


Fig 29

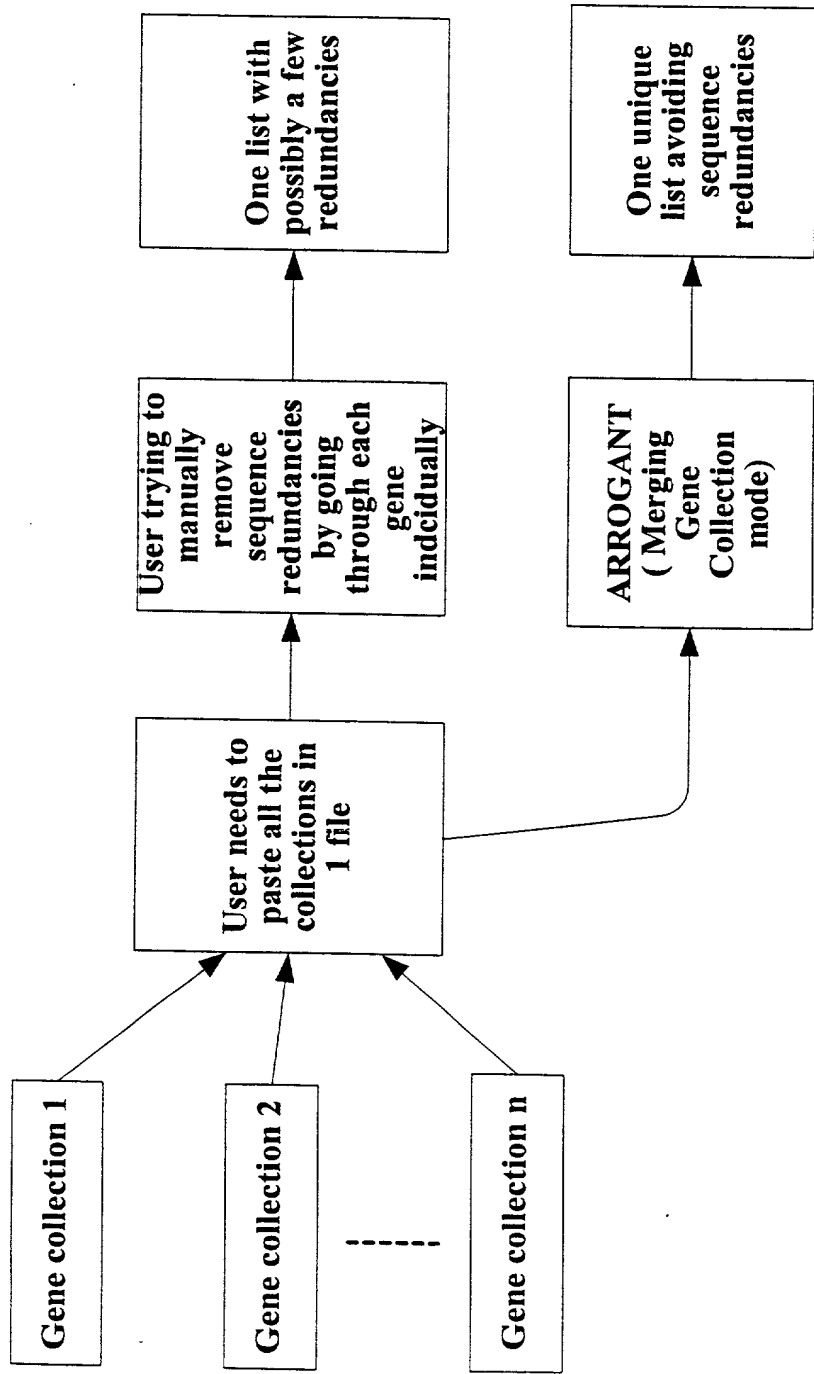


Fig 30

```
graph LR; A[Microarray results] --> B[Researcher interprets the results]; A -.-> C["ARROGANT (analysis mode) tags the potential false positives caused due to cross-hybridization"]; C -.-> B;
```

The flowchart illustrates the process of the ARROGANT analysis mode. It starts with a box labeled "Microarray results". A solid arrow points from this box to a box labeled "Researcher interprets the results". A dashed arrow points from "Microarray results" down to a box labeled "ARROGANT (analysis mode) tags the potential false positives caused due to cross-hybridization". A dashed arrow then points from this box up to the "Researcher interprets the results" box, indicating a feedback loop.

Fig 31a

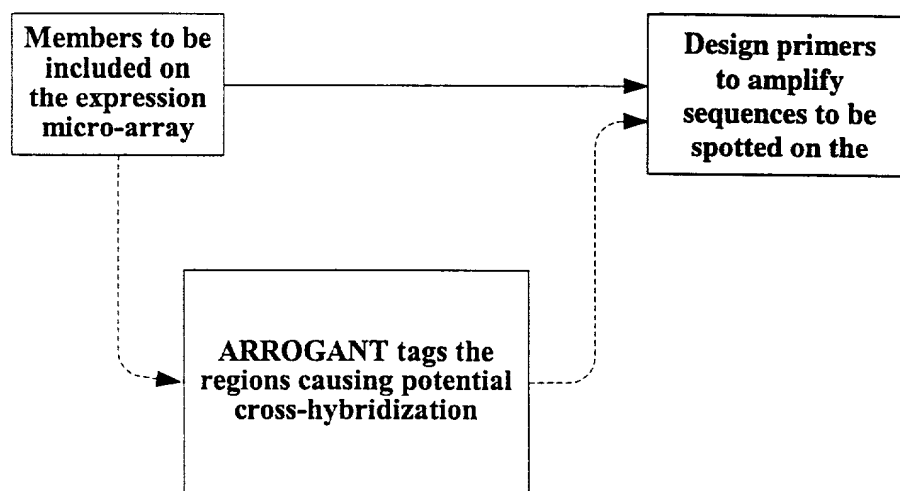


Fig 31b